

**IN THE CLAIMS:**

Please cancel claims 29 and 30 and replace with the following new claims:

~~31. (New) A gene that controls sucrose-starch metabolism comprising a nucleotide sequence comprising SEQ ID NO:9.~~

~~32. (New) A protein that controls sucrose-starch metabolism comprising a derived amino acid sequence comprising SEQ ID NO:10.~~

**REMARKS**

The above amendatory action has been taken in conjunction with Applicants' submission of a computer readable form copy and a paper copy of the Sequence Listing to comply with the requirements of 37 CFR 1.821 - 1.825. A marked up copy of the specification to locate the amendments thereto is attached.

Applicants submit herewith a statement that the contents of the paper copy and the computer readable copy are the same and include no new matter. In this latter connection, Applicants note that an obvious error in SEQ ID NO.9 has been rectified by adding a single nucleotide "G" at position 41. This correction does not constitute "new matter" in accordance with the provisions of MPEP Section 2163.07 (II). (An amendment to correct an obvious error does not constitute new matter where one skilled in the art would not only recognize the existence of error in the specification, but also the appropriate correction. *In re Oda*, 443 F.2d

1200, 170 USPQ 260 (CCPA 1971).").

The existence of the error in the specification and the appropriate correction would have been recognized by one skilled in the art from a comparison of Tables 6 and 7 on page 14 of the specification as filed. The nucleotide sequence of Table 6 is the nucleotide sequence of ADPGPPase LS1 from *L. hirsutum*. The amino acid sequence of Table 7 is the *derived* amino acid sequence of ADPGPPase LS1 from *L. hirsutum*, as stated, for example, on pages 13 and 14 of the specification as filed. The first 13 amino acids of the derived amino acid sequence in original Table 7 are the amino acids that are formed from the codons represented by the nucleotides at positions 1 - 39 of original Table 6. However, in order for amino acid 14 of the amino acid sequence of Table 7 to be "G" (glycine), the codon encoding the amino acid would have to be "GGU", "GCU", "GGA" or "GGG" (see Table of Codons submitted herewith). Since a review of Table 7 shows that the nucleotides are arranged in groups of ten (10) and that the group beginning with the nucleotide at position 41 contains only nine (9), it would be clear to one skilled in the art that this group is missing a nucleotide. It would also be clear that the missing nucleotide would have to be a "G" (guanine) for there to be correspondence between the codon at positions 40 - 42 of the nucleotide sequence of Table 6 and the amino acid at position 14 of the amino acid sequence of Table 7. Indeed, it is impossible to derive the amino acid sequence of Table 7 from the nucleotide sequence of Table 6 without the "G" at position 41. Furthermore, in the absence of the "G" at position 41, the nucleotide sequence of SEQ ID No. 9 is a probably meaningless truncated 26 amino acid protein.

By this amendatory action, Applicants have complied with all applicable requirements in the aforementioned Official Action. An early examination of this application on its merits is

respectfully requested.

Respectfully submitted,

CLIFFORD J. MASS  
LADAS & PARRY  
26 WEST 61ST STREET  
NEW YORK, NY 10023  
REG. NO. 30,086 (212) 708-1890

100-21500-20000-10000

c:\docs\13220amd.jun

Table 3-6 The Genetic Code

Second Position						Third Position
	U	C	A	G		
U	UUU Phe	UCU	UAU Tyr	UGU Cys	U	Third Position
	UUC	UCC Ser	UAC	UGC	C	
	UUA	UCA	UAA Stop	UGA Stop	A	
	UUG	UCG	UAG Stop	UGG Trp	G	
C	CUU	CCU	CAU His	CGU	U	Third Position
	CUC	CCC	CAC	CGC	C	
	CUA	CCA	CAA Gln	CGA	A	
	CUG	CCG	CAG	CGG	G	
A	AUU Ile	ACU	AAU Asn	AGU Ser	U	Third Position
	AUC	ACC	AAC Asn	AGC Ser	C	
	AUA	ACA	AAA Lys	AGA Arg	A	
	AUG Met	ACG	AAG Lys	AGG Arg	G	
G	GUU	GCU	GAU Asp	GGU	U	Third Position
	GUC	GCC	GAC Asp	GGC	C	
	GUU	GCA	GAA Glu	GGA Gly	A	
	GUG	GCG	GAG Glu	GGG	G	

Health in Bethesda, Maryland, observed, also in 1961, that the addition of the synthetic polynucleotide poly U (UUUUU . . . ) to a cell-free system capable of making proteins leads to the synthesis of polypeptide chains containing only the amino acid phenylalanine. The nucleotide groups UUU thus must specify phenylalanine. Use of increasingly more complex, defined polynucleotides as synthetic messenger RNAs rapidly led to the identification of more and more codons. Particularly important in completing the code was the use of polynucleotides like AGUAGU, put together by the Indian organic chemist H. G. Khorana, then working in Madison, Wisconsin. Completion of the code in 1966 revealed that 61 out of the 64 possible permuted groups corresponded to amino acids, with most amino acids being coded by more than one nucleotide triplet (Table 3-6).

### Start and Stop Signals Are Also Encoded Within DNA<sup>56-59</sup>

Initially, it was guessed that translation of an mRNA molecule would commence at one end and finish when the entire mRNA message had been read into amino acid sequences. But, in fact, translation both starts and stops at internal positions. Thus, signals must be present within DNA (and its mRNA products) to initiate and terminate translation. First to be worked out were the stop signals. Three separate codons (UAA, UAG, and UGA), first known as **nonsense codons**, do not correspond to any amino acids but instead serve as chain-termin-